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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 100243

TO: Vanessa L Ford

Location: cm-1/8A16/8E12

Art Unit: 1645

Aug 4____, 2003

Case Serial Number: 10/017168

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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From: Sent:

Chan, Christina

To: Subject:

Thursday, July 31, 2003 3:35 PM Ford, Vanessa; STIC-Biotech/ChemLib RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Ford, Vanessa

Sent:

Thursday, July 31, 2003 2:49 PM

To:

Chan, Christina

Subject:

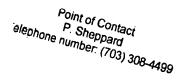
In re: 10/017168 sequence search

Please search SEQ ID NO:15. Please include interference searches. Please rush!

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8A16 Mailbox: CM1 8E12 Phone: 703.308.4735



Searcher:	
Phone:	
Location:	
Date Picked Up:	
Date Completed:	14/03
Searcher Prep/Revi	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
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VENDOR/COST (where app	lic.)
STN:	
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Questel/Orbit:	
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Q20072 caenorhabdi	Q20072	v	873	44.6	45	44
045181 caenorhabdi	045181	Ŋ	798	7	45	43
Q9jgt4 northern ce	Q9JGT4	12	483	44.6	45	42
Q96ys8 sulfolobus	Q96YS8	17	474	44.6	45	41
Q9gll3 macropus ru	Q9GL13	σ	379	44.6	45	40
_	Q9FFT7	10	294	44.6	45	39
Q817t9 arabidopsis	Q8L7T9	10	286	44.6	45	38
σ	Q9ANA3	N	286	44.6	45	37
O31775 bacillus su	031775	16	264	44.6	45	36
Q8pqy1 xanthomonas	QBPQY1	16	193	44.6	45	35
Q92ub5 rhizobium m	Q92UB5	16	178	44.6	45	34
Q23794 chironomus	Q23794	տ	99	44.6	45	ω W
Q23793 chironomus	Q23793	ຫ	99	44.6	45	32
Q8bkk6 mus musculu	Q8BKK6	11	853	45.5	46	31
Q8cjc3 mus musculu	QBCJC3	11	853	45.5	46	30
mus	Q8CG01	11	849	45.5	46	29
Q9h348 homo sapien	Q9H348	4.	779	45.5	46	28
Q93x74 brassica ra	Q93X74	10	434	45.5	46	27
Q93cv7 lactobacill	Q93CV7	N	383	45.5	46	26
Q8n446 homo sapien	Q8N446	4.	348		46	25
Q8w325 oryza sativ	Q8W325	10	174	45.5	46	24
Q9lp09 arabidopsis	Q9LP09	10	946	46.0	46.5	23
Q9c0a3 homo sapien	Q9C0A3	4.	1386	46.5	47	22
Q9imx8 cercopithic	Q9IMX8	12	1159	46.5	47	21
Q9xur2 caenorhabdi	Q9XUR2	v	1151	46.5	47	20
	Q9U381	տ	685	46.5	47	19
Q8iy36 homo sapien	QBIY36	4.	650	46.5	47	18
Q98494 paramecium	Q98494	12	308	46.5	47	17

ALIGNMENTS

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Q9ALV7
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Matches 20
                                                                                                  Liu H., Steiner B.;

"Acidic repeat protein (arp) gene sequence of Treponema pallidum subspecies pertenue (CDC 2 strain).";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF342806; AAK01460.2; -.

SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF411126; AAL07373.1; -.
SEQUENCE 107 "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
01-DEC-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                 Liu H., Steiner B.;

"Acidic repeat protein (arp) gene sequence of Treponema subspecies endemicum (Bosnia strain).";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL, AF342807; AAK01461.2;
 01-JUN-1998
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STRAIN=Bosnia;
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Bacteria; Spirochaetes; Spirochaetales;
NCBI_TaxID=53436;
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"Molecular characterization
Treponema pallidum.";
Submitted (SEP-2001) to the
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RESULT 6
OB3448
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Best Local S
Matches 20
                                                                                                                                                                                         O83448 PRELIMINARY;
O83448;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q93CA4
Q93CA4;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steiner B.M., Liu H., "Characterization of a pallidum.";
                                                                                      Treponema pallidum.
Bacteria; Spirochaetes;
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum subsp. pallidum (syphilis treponeme).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae;
NCBI_TaxID=161;
SEQUENCE FROM N.A.
STRAIN-Nichols;
MEDLINE-98323770; PubMed-9665876;
Fraser C.M., Norris S.J., Weinsto
                                                                                                                                                     Hypothetical TP0433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treponema pallidum.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF411124; AALO7372.1;
SEQUENCE 548 AA; 59405 MW; 1F6B5BBB04D41D13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Bacteria; Spirochaetes;
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01-OCT-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Nichols;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu H., Steiner B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                         168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF015824; AA
NCE 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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llarity 100.0%;
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TP0433
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Acidic 1
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Pred. No. 2.8e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 2;
Pred. No. 3.6e-07;
; Mismatches 0;
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Weinstock

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RESULT
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ID Q9
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Best Local S
Matches 17
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Best Local
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                       Q9SIJ8
Q9SIJB;
Q9SIJB;
01-WAY-2000
01-JUN-2002
01-OCT-2002
Expressed pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 281:375-388(1998).
EMBL; AE001220; AAC65421.1; -.
TIGR; TP0433; -.
Hypothetical protein; Complete
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MEDLINE=98332770;
  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 281:375-388(1998).
EMBL; AE001220; AAC65422.1;
TIGR; TP0434; -.
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Bacteria; Spirochaetės;
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Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Harch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter J.C.
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                                                                                                                                                                                                                                                                                                   EVEDVPGVVEPASGHEGGER
                                                                                                                                                                                                                                                                                                                                          EVEDVPKVVEPASEREGGER
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                                              protein
                                              ) (TrEMBLrel. 13, (2) (TrEMBLrel. 21, 12) (TrEMBLrel. 22, 12) (TrEMBLrel. 22, 13) protein (RD2 protein)
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256 AA; 27453 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l protein; Complete proteome.
227 AA; 25035 MW; 3FA02711A86E45FE
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                                                                                                                                                                         PRELIMINARY;
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rel. 20,
rel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%;
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95.0%;
                                           21, Last sequence update)22, Last annotation updat protein)
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Last annotation update)
                                                                                                                     Created)
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Pred. No. 0.00
0; Mismatches
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01-DEC-2001
01-DEC-2001
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Submitted (FEB-2002) to the EMBL/GenBank/DDE
                                                                                                                   Yamaguchi-Shinozaki K., Koizumi M., Urao S., Shinozaki K.; "Molecular cloning and characterization of 9 cDNAs for genes that are responsive to desiccation in Arabidopsis thaliana: sequence analysis
                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006016; Usp_dom. Pfam; PF00582; Usp; 1. SEQUENCE 187 AA; 20587 MW;
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Feldmann K.A., Flavell R.B.
"Full-length messenger RNA
annotation.";
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 Pfam; PF00582;
SEQUENCE 193
                                                   Plant Cell Physiol. 33:217-224(1992)
EMBL; AB039925; BAB63912.1; -.
                                                                                   protein.";
                                                                                                    of one cDNA clone that
                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Columbia;
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                     RD2 protein.
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Brover V., Troukha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biol. 0:0-0(2002).
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                                                                                                                                                                           STRAIN=Columbia;
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                                InterPro;
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                                IPR006016;
                                                                                                                                                                                                                              K., Yamaguchi-Shinozaki K., Takahashi S.; (MAR-2000) to the EMBL/GenBank/DDBJ databases
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White O., Salzberg S.L.;
sequences greatly improve genome
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21253 MW;

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A Strausberg R.;

L Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC018938; AAH18938.1; -.

R InterPro; IPR000345; CytC heme bind.

R InterPro; IPR002219; DAG PE-bind.

R InterPro; IPR002141; Znf ring.

R InterPro; IPR001841; Znf ring.

R ROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00181; DAG PE BIND DOM 2; 1.

DR PROSITE; PS50081; DAG PE BIND DOM 2; 1.

SO SEQUENCE 256 AA; Z9724 MW; 3433001005D7EDDF CRC64;
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Best Local
                           MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 58.3 kDa protein (Phosphoglucomutase).
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Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=H37Rv;
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01-MAY-1997
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01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2003 (TrEMBLrel. 23, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB Pred. No. 18; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 193;
                                                                                                                                                                                                                                                                                                                             Harris D.,
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RESULT 13
Q8CPY0
ID Q8CPY
AC Q8CPY
DT 01-M2
DT 01-M2

Q8CPY0; Q8CPY0; 01-MAR-2003 01-MAR-2003

(TrEMBLrel. (TrEMBLrel.

23,

Created) Last seq

sequence update)

PRELIMINARY;

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RESULT 12
Q8IBW7
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Best Local S
Matches 9
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Best Local S
Matches 10
                                                                                Seeger K., ru-, Seeger K., Barrell B.;
Quail M., Barrell B.;
Quail M., Barrell B.;
Cubmitted (SEP-2002) to the EN
Submitted (SEP-2002) to the EN
SEMBL, ALB44506; CAD50877.1; -
SEE CONTRICE 2192 AA; 248940 N
                                                                                                                                                                                                                                                       Q8IBW7;
Q8IBW7;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00408; PGM_PMM; 1.
Pfam; PF02878; PGM_PMM I; 1.
Pfam; PF02879; PGM_PMM_II; 1.
Pfam; PF02880; PGM_PMM_III; 1.
PTIGRERAMS; TIGR01132; PGM; 1.
PROSITE; PS00710; PGM_PMM; 1.
PROSITE; PS00710; PGM_PMM; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete S47 AA; 58265 MW; 1825BDDE89A9E951 CRC64;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=36329;
                                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                  Erythrocyte MAL7P1.56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TubercuList; Rv3068c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; MT3153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE007132; AAK47488.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
 877
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                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; IPR005841; PG/PMM mutase.
5; IPR005852; Pglucomut A.
5; IPR005844; PG PMM ABAII.
6; IPR005845; PG PMM ABAII.
6; IPR005846; PG PMM ABAIII.
6; IPR005846; PG PMM C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                          VDDLPNVVDIAAIREAGVR
EEKEAPKVVEPAVKKE
            EVEDVPKVVEPASERE 16
                                                                                                                                                                                                                                                                                                                                                                                                  VEDVPKVVEPASEREGGER
                                                                                                                                                                                                                                                       3 (TrEMBLrel. 23,
3 (TrEMBLrel. 23,
3 (TrEMBLrel. 23,
                                                                                                                                                                                                                                            membrane protein
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                                                  Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                          47.5%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%;
                                                                                                                                                       Harris
 892
                                                                                          O MW;
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                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                        Last
                                                 Score 48; DB
Pred. No. 2.5e
4; Mismatches
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
1 (PfEMP1).
                                                                                                                                                     D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                    4EAD66FF62A81329 CRC64;
                                                                                                                                                       Berriman M.,
                                                                                                                                                                                                                                                                                                           2192
                                                                             DB
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                                                                .5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                             databases.
                                                                                                                                                     Pain A.,
                                                                         Length 2192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 547;
                                                                                                                                                       Hall
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Mikula A.,
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                                                  Gaps
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RESULT 14
Q9D720
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  Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D720;
01-JUN-2001
01-JUN-2001
                                                                             InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR002219; DAG_PE-bind.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS500181; DAG_PE_BIND_DOM_2; 1.
SEQUENCE 266 AA; 30708 MW; F5728C530532E03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016745; AA004162.1; -.
                                                                                                                                                                                             EMBL; AK009715; br
MGD; MGI:1914961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Tongue; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9D720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 792 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacil
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribonuclease R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                           Nature 409:685-690(2001)
                                                                                                                                                                                                                                                            Hayashizaki Y.; "Function of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2510027N19Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235
                                                                                                                                                                                                 AK009715; BAB26459.1; -.
GI:1914961; 2510027N19Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              بر
  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAEEVPDVIEP-SEIEG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%;
                     46.5%;
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17,
23,
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Pred. No. 1e+0
2; Mismatches
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Last annotation update)
Score 47; DB
Pred. No. 38;
2; Mismatches
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2
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                     DB 11;
38;
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                                                                                                                                                                                                                                                                   mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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••
                                                                                                                                                                                                                                                                   cDNA collection.";
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                                          Length 266;
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RESULT 15
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ID Q8K2E
Search completed: August
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Matches 8
                                                                                                                               Straubberg R.;
Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031848; AAH31848.1; -.
InterPro; IPR003145; Cytc heme_bind.
InterPro; IPR002219; DAG PE-bind.
PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS00181; DAG PE BIND DOM 2; 1.
SEQUENCE 280 AA; 3Z038 MW; CC5BCCC949EA269F CRC64;
                                                                                                                                                                                                                                                                                                                                     Q8K2B4;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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           2003, 18:36:13
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Listing first 45 summaries
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Perfect score:
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      seq length: 0
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Match Length
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     SwissProt_41:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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ME31_DROWE
PPGA HUMAN
UL52_HCWMA
IILVB_ARATH
GAC1_YEAST
DPOL_ADB40
NEST_RAT
PSE1_MACFA
RS14_PROCL
CYNS_ECOST
YCEN_BCOLI
YC
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INTR SACER
VP41 HUMAN
VG72 HSV11
TRPC HALVO
CREM CUMPA
CREM CHOMAN
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Q03061
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P22877 saccharopol
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SEQUENCE Query Match Best Local S Matches 12 1	This SWISS-PF between the between the the Buropean use by non modified and entities requ or send an en EMBL; AE00086 PIR; B69215; Hypothetical	SEQUENCE STRAIN=E MEDLINE- Smith D. Smith D. Aldredge Harrison Spadafor Spadafor Jiwani N. McDougal Daniels "Complet deltaH: J. Bacte	SULT 1 7862 METTH 7862 METTH 7862 METTH 026950; 16-OCT-20 16-OCT-20 16-OCT-20 16-OCT-20 Methanoba Archaea Methanoba NCBI_TaxI	34 42 41 35 41.5 41 37 41.5 41 40 41 40 41 40 41 40 42 41 40 42 41 40 42 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 41 40 40 41 40 40 41 40 40 41 40 40 41 40 40 40 40 40 40 40 40 40 40 40 40 40
16874 MW; 51.0%; 63.2%; vative 3 EPASEREGGE EDALB-EGGE	cop cute lcs. itu itu int nse nse nse nse nse nse	Pelta H; R., Doucette-Stamm L.A., T., Bashirzadeh R., Blak D., Hoang L., Keagle P., a R., Vicare R., Wang Y., a R., Vicare R., Wang Y., I., Caruso A., Bush D., Sa I. S., Shimer G., Goyal A. C.J., Mao JI., Rice P., re genome sequence of Meth functional analysis and c functional analysis and c riol. 179:7135-7155 (1997) LARITY: TO M.JANNASCHII M	TH W	.6 1066 1 C5 .6 2329 1 Y1 .1 289 1 Z1 .1 365 1 AR .1 683 1 AR .6 149 1 R1 .6 150 1 R2 .6 151 1 R2 .6 151 1 R2 .6 151 1 R2 .6 198 1 D3
	is produced ormatics and There are 1 cong as its coved. Usage (See http://)	peloughery C., Lee kely D., Cook R., Gi, Lumm W., Pothier B, Wierzbowski J., Gi afer H., Patwell D., Ch., Pietrovski S., Ch., Noelling J., Reeve hanobacterium thermocomparative genomics)	RD; PRT; 153 AA. Created) Last sequence update) Last annotation update) MTH862. moautotrophicum. a; Methanobacteria; Methanobacteriales Methanothermobacter.	C505_FUSOX YLJ6_CAEBL ZIPA_PSEAE RP1_SYNY3 AMPH_RAT R141_MAIZE R144_DROME RS14_DROME RS14_HUMAN DJC5_HUMAN DJC5_HUMAN ALIGNMENTS
; th 153; els 1; Gaps 1;	through a collaboration d the EMBL outstation - no restrictions on its content is in no way by and for commercial www.isb-eib.ch/announce/	Gilbert K., Frabhakar S., Church G.M., we J.N., we J.N.;	riales;	09y8g7 fusarium ox p34369 caenorhabdi Q9i3i5 pseudomonas F74707 synechocyst 008838 rattus norv p19950 zea mays (m p19951 zea mays (m p14130 drosophila p06366 homo sapien p13471 rattus norv Q29455 bos taurus Q9h3z4 homo sapien

RESULT 2
INTR SACER STANDARD;
ID INTR SACER STANDARD;
AC P22877;
DT 01-AUG-1991 (Rel. 19, Created)

437 AA

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RESULT
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Reful; M35138; AAA98345.1; -.
Reful; M35138; AAA98345.1; -.
DR InterPro; IPR002104; Phage integrase; 1.
Pfam; PF00589; Phage integrase; 1.
Pfam; PF00589; Phage integrase; 1.
STRANSIENT COVALENT LINKAGE TO DNA STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
29EED7108CC5AFBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                  Vacuolar assembly protein VPS41 homolog (S53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the EMURPHEAD BIOINFORMATICS Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the genetic elements required for site-specific integration of plasmid pSE211 in Saccharopolyspora erythraea.";

J. Bacteriol. 172:1877-1888(1990)
-!- FUNCTION: Is a recombinase (or integrase), catalyzing the cutting and rejoining of the recombining DNA molecules.
-!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
Sherrington
                                                                                     Radisky D.C., Snyder W.B., Emr S.D., Kaplan J.; "Characterization of VPS41, a gene required for vacuolar trafficking and high-affinity iron transport in yeast."; Proc. Natl. Acad. Sci. U.S.A. 94:5662-5666(1997).
                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90202705; PubMed=2180909; Brown D.P., Idler K.B., Katz L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.
                     MEDLINE=95319502; PubMed=7596406;
                                                                                                                                                                    MEDLINE=97303186; PubMed=9159129;
                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
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                                          TISSUE=Brain;
                                                                                                                                                                                         TISSUE=Heart
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                        EQUENCE OF 615-744 FROM N.A.
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(Rel. 41, Last annotation update)
 Rogaev E.I., Liang Y.,
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                                                                                                                                                                                                                                                               Chordata;
Primates;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                   854 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
 Rogaeva E.A.,
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RESULT 4 VG72_HSVJ

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VG72 HSVI1 Q00103; 01-DEC-1992

STANDARD;

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01-DEC-1992 01-DEC-1992

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24, Last sequence update)
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72 protein.

update)

Hypothetical

gene

[ctalurid herpesvirus 1

(Channel catfish virus) (CCV).
no RNA stage; Herpesviridae;

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                                                                                                                       Matches
                                                                                        Query Match
                                                                                                                                                                                                                                    SMART; SMO0299; CLH; 1.

SMART; SM00299; CLH; 1.

SMART; SM00184; RING; 1.

PROSITE; PS000518; ZF RING 1; FALSE NEG.

PROSITE; PS50089; ZF RING 2; 1.

Zinc-finger; Alternative splicing.

Zinc-finger; Alternative splicing.

RING-TYPE.
                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 375:754-760(1995).
-!- FUNCTION: REQUIRED FOR VACUOLAR ASSEMBLY AND VACUOLAR TRAFFIC-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Hair Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                               InterPro; IPR000547; Clathrin_repeat.
InterPro; IPR001841; Znf_ring.
Pfam; PF00637; Clathrin; 1.
                                                                                                                                                                                                                                                                                                                                                                         MIM; 605485; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005478; F:intracellular transporter activity; TAS.
GO; GO:0007034; P:vacuolar transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U87309; AAB47563.1; -.
EMBL; U87281; AAB47758.1; -.
EMBL; L40398; AAC42004.1; -.
Genew; HGNC:12713; VPS41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                             NIAMO
                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P49754-2; Sequence=VSP_006751, VSP_006752; SIMILARITY: BELONGS TO THE VPS41 FAMILY. SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P49754-1; Sequence=Displayed
                                                          Similarity 9; Conserv
                             EVEDVPKVVEPASEREGGE
ELHDVDKAIEFAKEQDDGE
                                                                                                                     736
854 AA;
                                                                                                                                                  615
                                                           Conservative
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744
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                                                                         45.5%;
                                                                                                                     98535 MW;
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                                                     4;
                                                                         Score 46;
Pred. No.
                             19
 694
                                                                                                                                    KQIS -> WHEG (IN REF. 2)
IPNLRDSLV -> DPQFERFLG (
                                                                                                                                                                             /FTId=VSP_006751.
Missing (in isoform Short).
                                                                                                                                                                                                          POLY-GLU.
D -> E (in isoform
                                                                                                                                                                FTId=VSP_006752
                                                                                                                       B30F64D1320B550D CRC64;
                                                           Mismatches
                                                                           31;
                                                                                         BB
                                                                                         <u>,</u>
                                                           6,
                                                                                         Length 854;
                                                                                                                                                                                                              Short).
                                                          Indels
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                                                                                                                                    REF.
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RESULT 5
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Best Local (
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P18304;
01-NOV-1990 (Rel. 1
01-NOV-1990 (Rel. 1
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no cestrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                          EMBL; M36177; AAA72862.1; PIR; C36044; C36044.
                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                              volcanii.";
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                MEDLINE=90370836; PubMed=2118654;
                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium volcanii (Haloferax volcanii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HALVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 1:
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SMART; SM00355; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M75136; AAA88174.1; -. PIR; G36793; G36793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92087490; PubMed=1727613; Davison A.J.;
HSSP; Q06121; 1A53.
HAMAP; MF 00134; -; 1.
InterPro; IPR003009; FMN enzyme.
InterPro; IPR001468; IGPS.
                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 186:9-14(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                         "Genes for tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indole-3-glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                        Jam W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ictalurid Herpes-like viruses
                                                                                                                                                                                                                  c. Natl. Acad. Sci. U.S.A. 87:6614-6618(1990).

CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O. PATHWAY: Tryptophan biosynthesis; fourth step.

SIMILARITY: BELONGS TO THE TRPC FAMILY.
                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1350 AA;
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41, Last annotation
phosphate synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147547 MW;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                         biosynthesis
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                         the
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                                                                                                                 noved. Usage by and for commercial (See http://www.imb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
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Best Local
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HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD001511; IGPS; 1.
PROSITE; PS00614; IGPS; 1.
Tryptophan biosynthesis; Lyase;
SEQUENCE 251 AA; 26754 MW: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREM_HUMAN STANDARD; PRT; 332 AA (203060; Q16114; Q16116; Q9NZB9; Q1-JUN-1994 (Rel. 29, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                         modulator (CREM) gene.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meyer T.E., Habener J.F.;
"Cyclic AMP response element binding protein CREB and modulator protein CREB are products of distinct genes.";
Nucleic Acids Res. 20:6106-6106(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-232 FROM Vouk K., Lalli E., Sche Komel R., Rozman D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human CREM gene: evolutionary conservation, chromosomal localization, and inducibility of the transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00218; IGPS;
                                                                                                                                                                                                                                                                                                                                                                       "Searching for mutations in the human cAMP responsive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masquilier D., Foulkes N.S., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94128610; PubMed=7916662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93096608; PubMed=1461747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Na
                                                                                                                                                                                                                                                               BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CYTRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM SUBUNIT: Binds DNA as a dimer (By similarity).
                                                                    PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY: Belongs to the bZIP family.
                                                                                                                  Name=Delta;
                                                                                                                                              Name=Gamma
                                                                                                                                                                                                         Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                              inducibility of the transcript."; Growth Differ. 4:931-937(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                responsive element modulator.
                                                                                                   IsoId=Q03060-3;
                                                                                                                                                                                        IsoId=Q03060-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                               IsoId=Q03060-4;
                                                                                                                                                          IsoId=Q03060-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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                                                                                                                             Sequence=Not described;
                                                                                                                                                                                      Sequence=Displayed;
                                                                                                   Sequence=Not described;
                                                                                                                                                          Sequence=VSP_000599, VSP_000600, VSP_000601;
                                                                                                                                                                                                                    splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                   S.W., Sassone-Corsi P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB
Pred. No. 18;
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CREM_CANFA
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Best Local Similarity
Matches 9; Conser
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GO; GO:0007165; P:signal transduction; TA
InterPro; IPR001630; Leuzip_CREB.
InterPro; IPR0013102; pKID.
InterPro; IPR004827; TF_bZIP.
Pfam; PF00173; pKID; 2.
Pfam; PF00173; pKID; 2.
PRINTS; PR00041; LEUZIPPRCREB.
SMARF; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z15159; CAA78858.1; -.
EMBL; S68134; AAC60617.2; -.
EMBL; S68271; AAC60616.2; ALT SEQ.
EMBL; AF213899; AAF68266.2; JOINED.
EMBL; AF212158; AAF68266.2; JOINED.
EMBL; AF213899; AAF68266.2; JOINED.
EMBL; AF213899; AAF68266.2; JOINED.
                                                                                                                                                                                                         P79145;
15-JUL-1998
15-JUL-1998
28-FEB-2003
WEULINGES, MIOT F.;

Uyttersprot N., Miot F.;

"Dog CREM transcription factors: cloning, tissue distribution,

"Dog CREM transcription factors: n;

identification of new isoforms.";

Biochem. Biophys. Res. Commun. 237:74-78 (1997).

Biochem. Biophys. Res. Commun. 237:74-78 (1997).

-i- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CR:
                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                              TISSUE=Thyroid;
MEDLINE=97410117; PubMed=9266832;
                                                                                                                                         Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                         CREM CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Repressor; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:2352; CREM.
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear
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                                                                                                                               NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA BIND
                                                                                                                                                                                               responsive element modulator.
                                                                                                                                                                                                                                                                                                                     131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Alternative splicing.
275 296 BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     DVPGVPKIEEERSEEEG 147
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332
332 AA;
                                                                                                                                                                                                        (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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332
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Pred. No. 24;
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N -> I (IN REF. 2).
A -> R (IN REF. 1).
VSVAG -> CSELR (IN REF. 2).
D -> DY (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_000600.
A -> T (in isoform Alpha).
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Missing (in isoform Alpha).
/FTId=vcp noneco
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          (CRE), A
CREM ALPHA
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                         AMPH CHICK
P50478;
                                                                                                                                                                                                                              01-OCT-1996
01-OCT-1996
15-SEP-2003
                                                                                                                                      Arie...
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Numbrasuria: Aves; Neognathae; Galliformes; Phasianidae; Phasiani
           Lichte B., Veh R.W., Meyer H.E., Kilimann M.W.; "Amphiphysin, a novel protein associated with sembo J. 11:2521-2530(1992).
                                                       SEQUENCE FROM N.A.
STRAIN=Tetra-hybrid; TISSUE=Forebrain;
MEDLINE=92331604; PubMed=1628617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a copyre the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50217; BZIF; 1.

PROSITE; PS00036; BZIF BASIC; 1.

Transcription regulation; DNA-binding; Activator; Repressor; Phosphorylation; Nuclear protein; Alternative splicing. Phosphorylation; Nuclear protein; Alternative splicing. DNA BIND 287 308 BASIC MOTIF (BY SIMILARITY).

DOMAIN 314 335 LEUCING-ZIPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00170; bZIP; 1.—
Pfam; PF02173; DKID; LEUZIPPRCREB.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X99115; CAA67563.1; -. PIR; JC5601; JC5601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphiphysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001630; Leuzip_CREB.
InterPro; IPR003102; pKID.
InterPro; IPR004827; TF_bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: STIMULATED BY PHOSPHORYLATION (BY
-!- SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Binds DNA as a dimer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
 FUNCTION: MAY PARTICIPATE IN MECHANISMS OF REGULATED EXOCYTOSIS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTIONAL RESPONSE,
                                                                                                                                                                                                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P79145-4; Sequence=Not described;
M: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P79145-3;
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9; Conserve
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(Rel.
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34, Last sequence 42, Last annotations
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52.9%;
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                                                                                                                                                                                                                              sequence update)
annotation updat
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Pred. No. 24;
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                              synaptic vesicles.";
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Best Local
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PIR; S22700; S22700.
InterPro; IPR003005; Amphiphysin.
InterPro; IPR003017; Amphiphysin_1.
InterPro; IPR006632; BAR.
InterPro; IPR004148; BAR_dom.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _METTH
SYV_METTH
026861;
15-JUL-1998
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat valy1-trnA synthetase (EC 6.1.1.9) (Valine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00721; BAR; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01251; AMPHIPHYSIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD003208; Amphiphysin_1; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03114; BAR; Pfam; PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=187420;
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SIMILARITY: Contains 1
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LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURF
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RESULT 10
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HSSP; P96142; IGAX.
InterPro; IPR002300; tRNA-synt_Ia.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002300; tRNA-synt_val.
Pfam; PF00133; tRNA-synt_t, 1.
PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCH7 HUMAN STANDARD; PRT; 1069 AA. 060245; 060246; 060247; Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
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J. Bacteriol. 179:7135-7155(1997).
-i- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosing the comparative trna(Val).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                       Genomics 49:458-461(1998).
                                                                                                                                                                                                                                                                                                                              superfamily.";
                                                                                                                                                                                                                                                                                                                                                           BH-protocadherin (PCDH7), a novel member of
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE=98277460; PubMed=9615233;
Yoshida K., Yoshitomo-Nakagawa K., Seki N., Sasaki M., Sugano
"Cloning, expression analysis, and chromosomal localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCDH7 OR BHPCDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protocadherin 7 precursor (Brain-heart protocadherin) (BH-Pcch).
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PROSITE; PS00178; AA_TRNA_LIGASE I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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ISOIG=U0042---,
Name=C; Synonyms=BH-Pcdh-c;
ISoId=060245-3; Sequence=VSP_000705, VSP_000706;
ISOId=060245-3; Sequence=VSP_000705, VSP_000706;
ISOId=060245-3; Expressed predominantly in bra
                                                                                              Event-Alternative splicing; Named isof
Name-A; Synonyms-BH-Pcdh-a;
IsoId-o60245-1; Sequence=Displayed;
Name-B; Synonyms-BH-Pcdh-b;
IsoId-060245-2; Sequence=VSP_000704;
                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
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Similarity 46.7%;
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"KMSKS" REGION.
ATP (BY SIMILARITY).
WW; B939720D6D8FF0DB (
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Pred. No. 64;
                                                                                                                                                                                                                       Named isoforms=3;
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-!- SIMILARITY: Contains 7 cadherin domains.

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RESULT 11
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ID DNM1_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00232; CADHERIN_1; 6.
PROSITE; PS50268; CADHERIN_2; 7.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T00041; T00041.
PIR; T00042; T00042.
HSSP; P15116; 1NCJ.
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EMBL; AB006756; BAA25195.1; -.
EMBL; AB006757; BAA25196.1; -.
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PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 602988;
GO; GO:0005887; C:integral
InterPro; IPR002126; Cadher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:8659; PCDH7.
MIM; 602988;
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                                                                                                                     VGDVPFQLKPASDTEGDQ
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                                                                                                                                                                                                                        Score 44;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                             MRLHPYITVFG --> PFRRVTFSVVSQPQDPHQGSLQSCYD
SGLEESETPSSKSSSGPRLGALPLPEDNYERTTPDGSVDSR
PLPDVALTGKCTRECDEYGHSDSCWMPVRTSPERKKSQPKL
STFMFVDERGSQEKLANGEAAIMGDENRNLLNKKLTSSYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (in isoform /FTId=VSP_000705.
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CADHERIN 6.
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                     PRT;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA methyltransferase GgaI) (MCMT) (M.GgaI).

MRETHYLT OR AIM.

Gallus Gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               PRINTS; PR00105; C5METTRFRASE.
SMART; SM00439; BaH; 2.
TIGREPAMS; TIGR00675; dcm; 1.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
Transferase; Methyltransferase; Transcription regulation; Repressor;
DNA-binding; Zinc-finger; Zinc; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96172572; PubMed=8586618;
Tajima S., Tsuda H., Wakabayashi N., Asaso A., Mizuno
                                                                                                        Repeat;
                                                                                                                                                                                                                        Pfam; PF01426; BAH; 2.
Pfam; PF00145; DNA methylase; 1.
Pfam; PF02008; zf-CXXC; 1.
                                                                                                                                                                                                                                                           PIR; JC4172; JC4172.
REBASE; 3020; M.GgaI.
InterPro; IPR00125; BAH.
InterPro; IPR001525; C5_DNA_meth.
InterPro; IPR002857; Znf_CXXC.
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97451025; PubMed=9302295; Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li "Human DNA-(cytosine-5) methyltransferase-PCNA complex as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and expression of a chicken DNA methyltransferase cDNA.";
J. Biochem. 117:1050-1057(1995).
                                                                                                                                                                                                                                                                                                                             EMBL; D43920; BAA07867.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH PCNA, AND MUTAGENESIS OF VAL-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcriptional repression by
                                      ; Phosphorylation.

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791
1011
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420
                                  BAH 2.
7.5 x 2 AA TANDEM REPEATS OF K-G.
POLY-SER.
    POLY-GLU.
PHOSPHORYLATION (BY SIMILARITY)
BY SIMILARITY.
                                                                                                        INTERACTS
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                                                                                                        HIIM
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a target for
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                                                                                                                                                                                         Pfam; PF00514; Armadillo_seg; SMART; SM00185; ARM; 5. PROSITE; PS50176; ARM_REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenmodified and this statement is not removed. Usage by
                                                                                                             DOMAIN
                                                                                                                                                                       Wnt signaling
                                                                                                                                                                                                                                                         EMBL; D38629; BAA07609.1; -. HSSP; Q02248; 3BCT. InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K., Weisburger J.H., Sugimura T., Nagao M.; "Specific 5'-GGA-3'-->5'-GGA-3'-->6'-GGA-3' mutation of the Apc gene in rat col tumors induced by 2-amino-1-methy1-6-phenylimidazo[4,5-b]pyridine."; Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley, and Fisch MEDLINE=95148647; PubMed=7846077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA cloning of the rat APC gene and Mamm. Genome 6:746-748(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugimura T., Nagao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Fischer 344/N; TISSUE-Brain; MEDLINE-96116966; PubMed-8563176; Toyota M., Ushijima T., Kakiuchi H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70478;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APC_RAT
                                                                  REPEAT
                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY). SIMILARITY: Contains 7 ARM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1 and participates in Wnt signaling. APC activity is correlated witts phosphorylation state (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       816
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                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDVPKVVEPASEREG 17
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                                                                                                                                                                       pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Α.
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                                                                                                                                                                                             ARM REPEAT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T., Kakiuchi H., Watanabe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.6%;
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                                                                                                                                                                       Anti-oncogene;
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COILED CO
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ARM 2.
ARM 3.
ARM 4.
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Pred. No.
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                                                                                                                                                                                                                                     4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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(APC protein).
                                                                                       COIL
                                                                                                           COIL
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                                                                                                                                                                       Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assignment to chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
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                                                                                    (POTENTIAL)
                                                                                                        (POTENTIAL)
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                                                                                                                                                                       Coiled
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RESULT 13
CREM MOUSE
ID 701-81
DT 01-81
DT 01-81
DT 28-F1
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Best Local
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01-AUG-1992
01-AUG-1992
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM TAU).
MEDLINE=92114938; PubMed=1370576;
Foulkes N.S., Mellstroem B., Benusiglio E., Sa
"Developmental switch of CREM function during
antagonist to activator.";
Nature 355:80-84(1992).
-!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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REPEAT
DOMAIN
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA; MEDLINE=91145994; PubMed=1847666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foulkes
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                                                                                                         ISOId=P27699-4; Sequence=VSP_000602, VSP_000605, DEVELOPMENTAL STAGE: IN PREMEIOTIC GERM CELLS, EXPLANOUNTS IN THE ANTAGONIST FORM. SUBSEQUENTLY, DURIN SPERMATOGENESIS, THE ISOPORM TAU (ACTIVATOR) IS GENERAL AND IN EXTREMELY HIGH AMOUNT.

PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                  PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESPONSE, WHILE ISOFORM TAU IS AN SUBUNIT: Binds DNA as a dimer (By SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                     Name=Alpha;
IsoId=P27699-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. ISOFORD ALPHA, BETA, AND GAMMA ARE ANTAGONISTS OF THE CAMP TRANSCRIPT
                                                                                                                                                                                                                                                 Name=Gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1450
                                                                                                                                                                                                                                                                                                                                                                                                              Name≃Tau;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                    IsoId=P27699-3;
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P27699-1; Sequence=Displayed;
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10; Conserv
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ene: use of alternative DNA-binding d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P27698;
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(Rel. 23, Last sequence up)
(Rel. 41, Last annotation)
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                                                                                                                                                                                                                                                                                                              Sequence=VSP_000602, VSP_000603, VSP_000607;
                                                                                                                                                                                                                                                                    Sequence=VSP_000602,
                                                                                                                                                                                                                                                                                                                                                                                                                              splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARM 5.
ARM 6.
ARM 7.
SER-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
C-SE: IN AN IQ-INDUCED COLON TUMOR.
C-SR: IN AN IQ-INDUCED COCON TUMOR.
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Pred. No. 2.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Named isoforms=4;
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                                                                                                                                                                                                                                                                    VSP_000603,
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                                                                                                                                                                                                                                                                 VSP_000604;
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Best Local S
Matches 8
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InterPro; IPR003102; pKID.
InterPro; IPR004827; Tr_bZIP.
Pfam; PF00170; bZIP; 1.
Pfam; PF00173; pKID; 1.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M60285; AAA17495.1; -.
EMBL; M60285; AAA17496.1; -.
EMBL; M60285; AAA17497.1; -.
PIR; A37944; A37944.
PIR; B37944; B37944.
PIR; C37944; C37944.
PIR; C30827; S20827.
                                                                                     CREM RAT
Q03061;
01-JUN-1994
01-JUN-1994
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01310; --
TRANSFAC; T01314; --
TRANSFAC; T01315; --
TRANSFAC; T01316; --
TRANSFAC; T01602; --
TRANSFAC; T02108; --
TRANSFAC; T02109; --
                                                                                                                                                                                                    LT 14
_RAT
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD;
                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Nuclear DNA_BIND 284 305 DOMAIN 311 332 VARSPLIC 39 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP BASIC; 1.
Transcription regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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GO:0005667; C:transcription factor complex; IDA
                                                                responsive
                                                                                                                                                                                                                                                                                              128
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                              DVPGIPKIEEEKSEEEG
                                                                                                                                                                                                                                                                                                                                     EVEDVPKVVEPASEREG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
                                                                (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
sive element modulator.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                               STANDARD;
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Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   42.6%;
47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Alternative
BASIC MOTIF.
                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                   Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform Alpha, isoform and isoform Gamma).
/FTId=VSP_000602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKDICSP
KTD -> RECRRKKKEYVKCLENRVAVLENQNKTLIEELKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKDLYCHKAE (in isoform Alpha)
/FTId=VSP_000607.
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                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N (in isoform Alpha and isoform
                                                                                                                                                                               341 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing
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RESULT 15
RF2_CORGL
ID RF2_CORGL
AC Q8NS78;

STANDARD;

PRT;

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide chain release factor 2 (RF-2).

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Best Local :
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InterPro; IPR003102; p.
InterPro; IPR004000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meyer T.E., Habener J.F.;

"Cyclic AMP response element binding protein CREB and modulator ("Cyclic AMP response element binding protein CREB are products of distinct genes.";

Nucleic Acids Res. 20:6106-6106(1992).

1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA, BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.

1- SUBCULITIE BINDS BA dimer (By Similarity).

1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long 
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Activator; Repressor; Phosphorylation; Nuclear protein; Alternative splicing. DNA BIND 284 305 BASIC MOTIF (BY SIMILARITY). DOMAIN 311 332 LEUCINE-ZIPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00170; bZIP; 1.—
pfam; PF02173; DKID; 1.
PRINTS; PR00041; LEUZIPPRCREB.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z15158; CAA78857.1; -. PIR; S26686; S26686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93096608; PubMed=1461747;
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[1]
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=4;
128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P03069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q03061-4; Sequence=Not described; M: STIMULATED BY PHOSPHORYLATION (BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q03061-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q03061-1; Sequence=Displayed;
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                                                                                                   Similarity
8; Conserv
DVPGIPKIEEEKSEEEG
                                                 EVEDVPKVVEPASEREG
                                                                                                                                                                                                           341 AA;
                                                                                                     Conservative
                                                                                                                                                                                                           36628 MW;
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                                                                                                                              42.6%;
47.1%;
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144
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                                                                                                                                                                                                           LEUCINE-ZIPPER (BY SIMILA; 1DE752148670125E CRC64;
                                                                                                                              Score 43; DB Pred. No. 34;
                                                                                                        Mismatches
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Best Local Similarity 50.0
Best Conservative
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RAMAP; MF 00094; -; 1.

RINTERPRO; IPR0005139; PCRF.

RINTERPRO; IPR000352; PEP_rel_factor_I.

RINTERPRO; IPR000374; PrfB.

R Pfam; PF003462; PCRF; 1.

R Pfam; PF003462; RF-1; 1.

R PTGRFAMS; TIGR00020; PrfB; 1.

R PROSITE; PS00745; RF PROK I; 1.

R PROSITE; PS00745; RF PROK I; 1.

R PTOCEIN biosynthesis; Complete proteome.

SEQUENCE 368 AA; 41137 MW; C94D86D050AC5230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Corynebacterium glutamicum (Brevibacterium flavum).

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FACTORS FAMILY.
                                                           75 IEDLPIMVELAEEEDG
                                                                             2 VEDVPKVVEPASEREG 17 : | | : | | : |
                                                                                                                                     42.6%; Score 43; DB 1; Length 368; 50.0%; Pred. No. 37;
                                                             90
                                                                                                                        4; Mismatches
                                                                                                                      4; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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96.0
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49.317 Million cell updates/sec
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valine-tRNA ligase
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Gwin)

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hypothetical protein TP0433 - syphilis spirochete
()Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
()Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
()Ante: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
()Accession: F71326

R, Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: F71326
                                                                                   A;Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65422.1; PID:g332271:
A;Experimental source: strain Nichols
C;Genetics:
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A;Experimental source: strain Nichols
C;Genetics:
                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-227 <COL>
                                                                                                                                                                                                                                                            R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G71326
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A; Residues: 1-256 < COL>
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Best Local S
Matches 19
   Query Match
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ilarity 95.0%;
Conservative
   81.2%;
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Pred. No. 2.8e
0; Mismatches
   Score 82;
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2.8e-07;
   DB
2;
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Length 227;
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RESULT 5
E70650
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein At2g21620 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A;Molecule type: A;MTH>
A;Residues: 1-153 <MTH>
A;Cross-references: GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB85360.1; PID:g262195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein MTH862 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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                 Nhosphoglucomutase (EC 5.4.2.2) pgmA
C7Species: Mycobacterium tuberculosis
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Best Local S
Matches 10
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Matches 17; Conserv
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Best Local
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Residues: 1-184 <STO>
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tive 0; Mismatches
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Pred. No.
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Pred. No. 1
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                                       (strain
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T24541
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T17946
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                                                                         A; Molecule type: DNA
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Best Local S
Matches 10
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Best Local :
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submitted to the EMBL Data Library, A,Reference number: Z18806 A;Accession: T17946 A,Stature
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C;Accession: E70650
C;Accession: E70650
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
Naturbors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70650
A; Residues: \bar{1}-1151 <WIL> A; Cross-references: EMBL: Z81586; PIDN: CAB04695.1; GSPDB: GN00019; CESP: T05F1.6a A; Experimental source: clone T05F1
                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19905 A;Accession: T24541
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C;Accession: T24541
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C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A443R
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                           hypothetical protein T05F1.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC968
A;Experimental source: specific host Chlorella strain NC64
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A; Residues: 1-308 < GRA>
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C;Species: Chlorella virus PBCV-1
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                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 21;
4; Mismatches
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                                                                                                                                                                                                                                                                                 15-Oct-1999 #text_change 15-Oct-1999
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C;Accession: Lyosus R; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Adu, C., Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; SChwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                         R;Brown, D.P.; Idler, K.B.; Katz, L.

J. Bacteriol. 172, 1877-1888, 1990
A;Title: Characterization of the genetic elements required for site-specific integration A;Reference number: A35147; MUID:90202705; PMID:2180909
A;Accession: C35147
                                                                                                                                                                                                                                                                                                                                                                    integrase homolog - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change
C;Accession: C35147
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A; Residues: 1-946 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein F9C16.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A;Map position: 1
A;Introns: 9/1; 21/2; 43/3; 186/3; 483/2; 574/3; 611/1; 957/3; 1029/2; 1124/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                       A;Cross-references: GB:M35138; NID:g152671; PIDN:AAA98345.1; PID:g152674
                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-437 <BRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005173; NID:g8778679; PIDN:AAF79687.1; GSPDB:GN00141
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                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                        Matches
                                                                                                                                Query Match
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185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVEDVPK----VVEPASEREGGER 20
                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 9; Conserv
                                                                                                           Similarity
EVEDMQLVIKAALERRNGVR 204
                                     EVEDVPKVVEPASEREGGER 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAEDVPQLVDVVQPKSNRKSRKR 46
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Pred. No. 63;
4; Mismatches
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                                                                                                        Score 46;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                      Mismatches
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64;
                                                                                                                             DB 2;
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                                                                                                                           Length 437;
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A;Molecule type: DNA
A,Residues: 1-91,'A',93-99 <CL2>
A;Cross-references: EMBL:Z36897; NID:g534886; PID:g534887
A;Experimental source: clone pCMG106
C;Genetics:
                       A;Cross-references: GB:AL591985; PIDN:CAC49621.1; PID:g15141108; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T. M; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: suggested by Southern blot analysis in Ref C;Keywords: chromosomal protein; DNA binding F;8-13/Region: DNA-binding motif (K/R-G-R-G-R-P) F;75-80/Region: DNA-binding motif (K/R-G-R-G-R-P) F;75-80/Region: DNA-binding motif (K/R-G-R-G-R-P)
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A; Accession: S47253
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R;Claus, P.; Schulze, E.; Wisniewski, J.R.
submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-178 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - C; Species: Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 15/3; 76/1
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A; Residues: 1-99 < CLA>
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A;Title: Insect proteins homologous to mammalian high mobility
A;Reference number: A55819; MUID:95105193; PMID:7806532
A;Accession: A55819
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R;Claus, P.; Schulze, E.; Wisniewsk
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A; Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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Pred. No. 10;
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44.68;

Score

45; DB 2;

Length 178;

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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Saddaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamanoto, K.; Yasumoto, K.; Yasua, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Scandard Complete Scandard General Complete School, Characterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                          R; Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, submitted to the EMBL Data Library, February 1998
A; Description: The sequence of C. elegans cosmid K07H8.
A; Reference number: Z21264
A; Accession: T33022
                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-798 <FUL>
A;Cross-references: EMBL:AF047659; PIDN:AAC04430.1; GSPDB:GN00022; CESP:K07H8.10
A;Experimental source: strain Bristol N2; clone K07H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä;Residues: Î-264 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13570.1; PID:g2634069
A:Experimental source: strain 168
                                                                                                     A; Map position: 4
A; Introns: 205/1; 308/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein K07H8.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                               A; Gene: CESP: K07H8.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not
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Best Loc
Matches
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8; Conserv
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                                                                                                        630/1; 773/3
                        44.6%;
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4; Mismatches
4.
                        Score 45;
Pred. No.
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Pred. No.
  Mismatches
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89;
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28;
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                                                 Length 798;
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Virology 186, 9-14, 1992
Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type
A;Title: Channel catfish virus: a new type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ORP72 - ictalurid herpesvirus 1 (strain auburn C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-h
C;Accession: G36793
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G36793
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F35H10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
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T16282
                                                                                                                                                                 C; Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF72
                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to GenBank, January 1992 A; Description: Channel catfish vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: vacuolar
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A; Introns: 39/3; 709/3;
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A; Residues: 1-873 <WOE>
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                                                                                                                                                                                                                             A; Note: neither protein nor nucleic acid sequence is giver
                                                                                                                                                                                                                                                 A; Contents: annotation
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A;Cross-references: GB:M75136; NID:g331209; PIDN:AAA88174.1; PID:g331280
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A36804
A; Accession: G36793
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9; Conserve
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9; Conservative 4...
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56.2%; Pred. No.
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PMID:1727613
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98;
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2003, 18:38:00

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 80
                                                                                                                                                                                                                                                                                                                                                    Score
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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101
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
        EVEDVPKVVEPASEREGGER
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/ Cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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                        15 US-10-036-542-66
15 US-10-036-542-92
15 US-10-036-542-134
15 US-10-036-542-130
10 US-09-864-761-3592
10 US-09-864-761-3592
10 US-09-764-864-1172
10 US-09-752-639-151
10 US-09-752-639-151
10 US-09-754-864-1091
11 US-09-784-1864-1091
11 US-09-784-1864-1091
11 US-09-784-65690
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Sequence 66, Appl
Sequence 134, Appl
Sequence 130, Appl
Sequence 1615, Appl
Sequence 35920, A
Sequence 1172, Appl
Sequence 1172, Appl
Sequence 151, Appl
Sequence 151, Appl
Sequence 151, Appl
Sequence 1501, Appl
Sequence 6590, Appl
Sequence 6590, Appl
Sequence 6590, Appl
Sequence 6590, Appl
Sequence 6350, Appl
Sequence 6350, Appl
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ALIGNMENTS

US-10-036-542-66

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; SEQ ID NO 66
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo 8
US-10-036-542-66
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TITLE OF INVENTION: 25 Human Prostate and Profile Reference: pA002p1
FILE REFERENCE: pA002p1
CURRENT APPLICATION NUMBER: US/10/036,542
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/US00/19666
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/144,972
PRIOR PILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 60/148,681
PRIOR APPLICATION NUMBER: 60/149,173
PRIOR APPLICATION NUMBER: 60/149,173
PRIOR APPLICATION NUMBER: 60/158,004
PRIOR APPLICATION NUMBER: 60/158,004
                                                                              Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/194,689 PRIOR FILING DATE: 2000-04-05
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  238 EIPKVFDPEKERESG 252
                                      4 DVPKVVEPASEREGG 18
                                                                              Similarity
8; Conser
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nilarity 53.3%;
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Pred. No. 12;
3; Mismatches
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                                                       SEQ ID NO 134
LENGTH: 277
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Publication No. US20
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US2
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CURRENT FILING DATE: 2002-01-07
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TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
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CURRENT FILING DATE: 2002-01-07
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PRIOR APPLICATION NUMBER: 60/149,173
PRIOR FILING DATE: 1999-08-17
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PRIOR FILING DATE: 1999-07-21
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PRIOR FILING DATE: 2000-07-20
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                                                                                               SOFTWARE:
                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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FEATURE:
                ORGANISM: Homo sapiens
                                    TYPE: PRT
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                                                   ENGTH:
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                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/149,173
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                                                                                                                                                                             FILING DATE:
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                                                                                             PatentIn
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53.3%;
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Pred. No. 13;
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1615
LENGTH: 304
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SEQ ID NO 130
LENGTH: 288
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Best Local Similarity
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                                                                                                                                                                                                                                                                                            Sequence 1615, Application US/09925300 Patent No. US20020151681A1
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CURRENT FILING DATE: 2002-01-07
CURRENT FILING DATE: PC7/US00/19666
PRIOR APPLICATION NUMBER: PC7/US00/19666
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/144,972
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PRIOR
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PRIOR APPLICATION NUMBER: 60/149,173
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PRIOR APPLICATION NUMBER: 60/148,681
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TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
                                                                                                                                                                                               FILE REFERENCE: PA101
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                                                                                                                                                                                                                 NPPLICANT: Steve Ruben
IITLE OF INVENTION: Nucleic Acids, Proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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LOCATION: (147)
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Pred. No.
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Best Local S
Matches .8
                                 SOFTWARE: Annomax
SEQ ID NO 35920
LENGTH: 71
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PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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                                                                                NUMBER OF SEQ ID NOS: 49117
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FEATURE:
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DRGANISM: Homo sapiens
                                                                                                                            FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 24263.6
                                                                                                                  APPLICATION NUMBER: US
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                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669
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US20020048763A1
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Chen, Wensheng
                                                                                                   DATE:
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                                                                                                                                                                                                                                                                                                                                                          NUMBER: PCT/US01/00665: 2001-01-30
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                                                               Sequence Listing
                                                                                                                                                                                                                                                                                                           NUMBER: PCT/US01/00663
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Pred. No.
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14;
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                                                                                               GENERAL INFORMATION:
                                                               APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
   APPLICANT:
                                   APPLICANT:
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RESULT 8
US-10-156-761-10989
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US-09-764-864-1172
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Sequence 10989, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1172, A
Patent No. US200
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Best Local
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo :
FEATURE:
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LOCATION: (262
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LOCATION: (58)
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0020132753A1
                                                                                                                                   Conservative
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EXPRESSED IN PLACES
EXPRESSED IN BRAIN
EXPRESSED IN ADULT
EXPRESSED IN FETAL
EXPRESSED IN BT474.
EXPRESSED IN HEART
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EXPRESSED IN HEART
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D IN HEART, SIGNAL = 1.7
D IN HELA, SIGNAL = 2.3
D IN HBL100, SIGNAL = 2.1
D IN LUNG, SIGNAL = 5.1
D IN BONE MARROW, SIGNAL = 2
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IN ADULT LIVER, SIGNAL =
IN FETAL LIVER, SIGNAL =
2.1
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Pred. No. 16;
4; Mismatches
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Pred. No.
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SHIBA, TADAYOSHI SAKAKI, YOSHIYUK ISHIKAWA, JUN HORIKAWA, HIROSHI

HATTORI,

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RESULT 9
US-09-752-639-151
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Best Local S
Matches 9
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LENGTH: 392
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
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CURRENT FILING DATE: 2002-05-29
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                                                      NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Garanger, G.A.
TITLE OF INVENTION: Factors Alterin
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                               TELEPHONE: 650-813-5600
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                                                                               TELEFAX: 650
TELEFAX: 706141
                                                                                              TELEPHONE: 650-02-0792
                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 755 PAGI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                    NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Window
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ZIP: 94304-1018
STRANDEDNESS:
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EVIDTPEAAREATERLGGK 41
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47.4%; Pred. No. 1.10
ative 3; Mismatches
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Query Match
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gatanaga, T.
APPLICANT: Granger, Gack.
TITLE OF INVENTION: Factor Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/9
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/0
FILING DATE: 06-NOV-1996
                                                                                                                                                                                                                                          TELEPHONE: 650-813-56
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                     NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
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CLASSIFICATION:
                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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APPLICATION NUMBER:
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 954
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EEVPEIQEKEEQEEGRER 971
                              EDVPKVVEPASEREGGER 20
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                                                                                                                                                                                  1038 amino acids
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                                                            43.6%; Score 44; DB 10; 44.4%; Pred. No. 3.2e+02; tive 4; Mismatches 6;
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Pred. No. 3
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                                                                                                                    US-09-738-626-6590
                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-764-864-1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1091, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 109
                                                                                        Sequence 6590, Application US/09738626 Publication No. US20020197605A1
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Best Local S
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                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: No. US20030104479Alel Fusion Proteins And Assays For Molecular Bi
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
                                                 APPLICANT:
                                                           APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/309,395 PRIOR FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                 LENGTH: 178
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Binding domain
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TYPE: PRT
ORGANISM: Artificial sequence
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8; Conserv
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8; Conserv
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     ANDO, SEIKO
HAYASHI, MIKIR
OCHIAI, KEIKO
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                                                MIZOGUCHI, HIROSHI
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Pred. No.
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Pred. No.
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17;
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RESULT 15
US-09-738-626-4393
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; Publication No. US20020197605A1
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US-10-102-806-605
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TYPE: PRT
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; ORGANISM: Corynebacterium glutamicum US-09-738-626-6590
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn ver.
SEQ ID NO 6590
LENGTH: 241
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SEQ ID NO 605
LENGTH: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 605, Application US/10102806
Publication No. US20030054421A1
                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo s
FEATURE:
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                       NAME/KEY: SITE LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                      Local Similarity
mes 9; Conserv
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                                 3 EDVPKVVEPASEREGG 18
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EDNPEVVRPHNGRVGG 155
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TATEISHI, NAOKO
                                                                        Conservative
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56.2%; Pred. No.
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Pred. No.
                                                                                          Pred. No. 97;
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87;
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GENNEAL INFORMATION:
APPLICANT: MIXOGUCH; HIROSHI
APPLICANT: MIXOGUCH; HIROSHI
APPLICANT: MIXOGUCH; HIROSHI
APPLICANT: MIXOGUCH; HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: CCHIAI, KEIKO
APPLICANT: CCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: OCAKI, AKIGH
APPLICANT: OCAKI, NASATO
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APICANT: OCA
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /cgn2_6/ptodata/1
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3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
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   EVEDVPKVVEPASEREGGER
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                           US-09-035-648-18
US-09-001-951-18
US-08-0818-829-18
US-08-363-208-2
US-09-117-478-2
US-09-117-478-2
US-09-137-478-2
US-09-367-512-7
US-09-367-512-7
US-09-33-750-45
US-09-234-613-45
US-09-234-613-45
US-09-199-637A-341
US-09-199-637A-341
US-09-199-637A-341
US-09-199-637A-341
US-09-199-637A-341
US-09-252-991A-21487
US-09-252-991A-21487
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US-09-252-991A-21490
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US-09-252-991A-32898
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US-09-163-748C-7
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29.180 Million cell updates/sec
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35, Appl
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2, Appl
1401, Ap
3411, Ap
21187, A
32102, A
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26148, A
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40.1	40.1	40.1	40.1	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6
98	59	59	.59	5215	1841	1018	1018	1018	749	510	464	388	349	313	256	151
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US-08-481-658B-50	US-09-177-776-50	US-09-178-115-50	US-08-787-739-50	US-09-105-537-2	US-08-804-227C-6	US-09-092-458-2	US-08-719-822B-2	US-08-072-610-2	US-09-562-737-98	US-09-252-991A-33084	US-09-252-991A-26212	US-09-252-991A-22751	US-09-252-991A-25831	US-09-252-991A-24305	US-09-252-991A-29587	US-09-732-210-1402
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
•		50, Appl	50, Appl	2, Appli	6, Appli	2, Appli	2, Appli	2, Appli	98, Appl	33084, A	26212, A	22751, A	25831, A	24305, A	29587, A	1402, Ap

ALIGNMENTS

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Sequence 5584, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOST
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5584
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US-09-163-748C-7
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US-09-134-001C-5584
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Matches
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GENERAL INFORMATION:
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SEQ ID NO 5584
LENGTH: 801
                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                   APPLICANT: DeBacker, Oliver
APPLICANT: Wan den Bynde, Benoit
APPLICANT: Wan den Bynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode Member Of The PITLE OF INVENTION: Family, The Proteins Encoded, And Uses Thereof
FILLE REFERENCE: LUD 5558
CURRENT APPLICATION NUMBER: US/09/163,748C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 27
TYPE: PRT
ORGANISM: Homo :
FEATURE:
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                                                        ENGTH: 117
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Pred. No. 22;
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                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-32898
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US-09-252-991A-26148
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                                                                    Best Loc
Matches
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                         SEQ ID NO 32898
LENGTH: 228
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Best Local
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SEQ ID NO 26148
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                                                                                                                                                                                                                         PILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1996-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1996-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION:
TITLE OF INVENTION:
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                           TYPE: PRT
                                                                                    Local
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VEHVPGVVEPLSRGHG 89
                                  VEDVPKVVEPASEREG 17
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WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                    Conservative
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46.7%;
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Pred. No. 21;
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                                                               Pred. No. 18;
0; Mismatches
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Pred. No.
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US-09-001-951-18
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                                                                                                                                                                                                     Sequence 18, Applicat Patent No. 6268470 GENERAL INFORMATION:
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NAME: Meiklejohn, Ph.D., An
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/035,648
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818,829
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                    APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSIT
TITLE OF INVENTION: DIAGNOSII
TITLE OF INVENTION: GROWTH A
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LENGTH: 747 amino acid
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                      NUMBER OF SEQUENCES:
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COUNTRY: US
ZIP: 02110-2804
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Local Similarity 50.0%;
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ZIP: 02110-2804
                                  STATE:
                                                                  STREET:
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TELEPAX: 617-542-8906
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                                                                                  ADDRESSEE:
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225 Franklin
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                                                                                   Richardson,
                                                                                                                                      GROWTH AND
                                                                                                                                                      COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION, AND TREAT!
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                                                                                                                                                                                                                                                                                                                                                                                         4;
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Pred. No.
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COMPUTER READABLE FORM:

COMPUTER: IBM CON OPERATING SYSTEM:

Diskette M Compatible TEM: Windows95

FastSEQ for Windows Version 2.0

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Query Match
Best Local Similarity
Marches 9; Conserva
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APPLICATION NUMBER: 08/818,829
FILING DATE: 14-MAR-1997
APPLICATION NUMBER: 60/013,438
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,438

PILING DATE: 15-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/0030
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TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,829
FILING DATE: 14-MAR-1997
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: COMPOSIT
TITLE OF INVENTION: DIAGNOSI
TITLE OF INVENTION: GROWTH A
NUMBER OF SEQUENCES: 24
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FRAGMENT TYPE:
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APPLICATION NUMBER: US
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CITY: Boston
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internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROWTH AND PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION, AND TREAT!
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     07334/003001
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                                Matches
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Best Local (
                                                                 Query Match
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                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sathasivan, APPLICANT: Murai, No. 5
TITLE OF INVENTION: A A TITLE OF INVENTION: Are TITLE OF INVENTION: Recommendation of SEQUENCES: 2
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Proctor Sr., Llewellyn A.
REGISTRATION NUMBER: 20,152
REFERENCE/DOCKET NUMBER: 013911
TELECOMMUNICATION INFORMATION:
                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 70815
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Llewellyn A. Proctor, Sr. STREET: 11481 Sheraton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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FRAGMENT TYPE:
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TELEFAX: v_
SEC
                                              Local Similarity
                                                                                                                                                                                                                   TELEPHONE:
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1 EVEDVPKVVEPA 12
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                                                                                                                                                              670 amino acids
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nilarity 50.0%;
Conservative
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                                Conservative
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internal
                                                                                                                                                                                                                 504) 275-8689
                                              42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Mutant Acetolactate Synthase Gene From
Arabidopsis Thaliana For Conferring Imidazolinone
Resistance To Crop Plants
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Pred. No. 72;
                                                Score 43; DB Pred. No. 91;
                                Mismatches
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                                Indels
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                                                                                                                                                                                                                                      Sequence 8, Approx. 10. 5853973
                                                                                                                                                                                                                        Patent No. 5853973
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
ATTORNEY/ACENT INFORMATION:
NAME: Proctor Sr., Llewellyn A.
REGISTRATION NUMBER: 20,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sathasivan, Kanagasabapathi
APPLICANT: Murai, No. 6225105:noto
TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene
TITLE OF INVENTION: Arabidopsis Thaliana For Conferring
TITLE OF INVENTION: Resistance To Crop Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                            APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
                                                                                                                                                             APPLICANT: Kakefuda, Genichi
APPLICANT: Ott, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
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                                                                      NUMBER OF SEQUENCES: 1
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Local Similarity 50.0%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
CITY: New York
STATE: New York
                                   STREET:
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REFERENCE/DOCKET NUMBER: 01:
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                                                       ADDRESSEE:
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                                   E: Darby & Darby
805 Third Avenue
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 670;
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                                                                                  ZIP: 10022-7513

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,355
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 236687
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acid
TYPE: amino acid
STRANDEDNESS:
ATTORNEY/AGENT INFORMATION:
NAME: RObinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A674-US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,125
FILLING DATE: 20-APR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: RObinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kakefuda, Genichi
APPLICANT: Ott, Karl-Heinz
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                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)-52,
TELEPHONE: (212)-753-6237
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                   STREET:
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o. 5928937
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amino acid
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Stockton, Gera
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                                                                                                                                                                                                                                                                                                                                                                                                              Resistant Products
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                                                                                                                                                                                                                                                                                                                                                                                             10
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Pred. No. 92;
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RESULT 13
US-09-046-894-35
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Matches 6; Conserv
                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7
                                                                                                                                                           Sequence 35,
                                                                                                                                                                                                                                                                                                                      Matches
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APPLICANT: Stockton, Gerald W.
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant
TITLE OF INVENTION: Products
FILE REFERENCE: 3489/1A674-US3
CURRENT APPLICATION NUMBER: US/09/367,512
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 08/426,125
PRIOR APPLICATION NUMBER: 08/455,355
PRIOR APPLICATION NUMBER: 08/455,355
PRIOR PILING DATE: 1995-04-20
PRIOR APPLICATION NUMBER: 08/455/355
PRIOR APPLICATION NUMBER: 08/455/355
PRIOR APPLICATION NUMBER: PCT/US96/05782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parent No. 6576455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: American Cyanamid Company
APPLICANT: Kakefuda, Genichi
APPLICANT: Ott, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu.
APPLICANT: Stockton, Gerald W.
                                                                                                       GENERAL INFORMATION: APPLICANT: Ralph,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1996-04-19
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Arabidopsis thaliana
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                                                   APPLICANT:
APPLICANT:
APPLICANT:
                APPLICANT: Veltri, Robert TITLE OF INVENTION: DIAGN TITLE OF INVENTION: PROFI
                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 671
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    Local Similarity les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 671 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                   1 EVEDVPKVVBPA 12
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DVEDIPRIIEEA 238
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                                                                                                                                                           Application US/09046894
                                                              An, Gang
O'Hara, Mark S.
                                                                                                   Ralph, David
                                                                                                                                                                                                                                                                                                                      Conservative
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                DIAGNOSIS OF DISEASE STATE USING MRNA PROFILES IN PERIPHERAL LEUKOCYTES
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Pred. No.
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Pred. No. 92;
                                                                                                                                                                                                                                                                                                                      Mismatches
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US-08-933-750C-45
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (512) 474-75
                                                                                                 COUNTRY: USA
ZIP: 94304
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
APPLICATION NUMBER: US/08/933,750C
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 761 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                   APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
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                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/046,894 FILING DATE: Concurrently Herewit: CLASSIFICATION:
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STATE: Texas
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ZIP: 77210
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Bandman, Olga
                                                                                    B: Diskette
IBM Compatible
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September 23, 1997
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

PF-0356 US

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 811 amino acid

45:

TELEFAX: 415-845-4166

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LENGTH: 811 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRTUTO4
CLOME: 2515476
US-08-933-750C-45
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Best Local Similarity
Marches 7; Conserve
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APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                            APPLICATION NUMBER:
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6132973
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Hillman, Jennifer L.
Bandman, Olga
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41.2%; Pred. No. 1.1e+02;
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                                                                                                                     US-09-234-613-45
                                                          Matches
                                                                                     Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 811 amino acids
                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: LIVRT
CLONE: 2515476
                                                         y Match 42.6%; Score 43; DB 3; Le Local Similarity 41.2%; Pred. No. 1.1e+02; hes 7; Conservative 4; Mismatches 6;
                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                             STRANDEDNESS:
777 DTPATSDPLSEEKGGKK 793
                            4 DVPKVVEPASEREGGER 20
                                                                                                                                                                                                           amino acid
                                                                                                                                                  LIVRTUT04
                                                                                                                                                                              linear
                                                                                                                                                                                             single
                                                                                                                                                                                                                                                           45:
                                                                                       DB 3; Length 811;
                                                            Indels
                                                            <u>,</u>
                                                            Gaps
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Search completed: August 1, 2003, 18:38:35 Job time : 30 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  August 1, 2003, 18:22:55; Search time 41 Seconds (without alignments) 77.428 Million cell updates/sec
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Gapop 10.0 ,
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AAi985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AAi986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-
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/SIDS1/gcgdata/geneseq/geneseqp-embl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22	222	22	2 2	22	22	B
AAB48330 AAB48321	AAB48328 AAB48320	AAB48329	AAB48318	AAB48317	AAB48327	ID
T. pallidum acidic T. pallidum acidic	pallidum pallidum	T. pallidum acidic	T pallidum ssp.en	pallidum	T. pallidum acidic	Description

Detecting Treponema pallidum in blood, saliva, etc., formation of a complex between immunogenic peptides of protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the

, by detecting of acidic repeat the biological

WPI; 2001-080711/09.

AAB48319 AAB48326 AAB61629 AAG61629 AAG6629 AAG850350 AAG86279 AAB80347 AAG81774 AAG81774 AAG81777 AAG867 AAG859486 AAG8693

ALIGNMENTS

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RESULT 1
AAB48327
Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                                                              21-DEC-2000.
                                                                                                                                               Treponema pallidum
                                                                                                                                                                                                       20-APR-2001 (first entry)
                                                                                                                                                                                                                        AAB48327;
                                                                                                                                                                                                                                       AAB48327 standard; peptide; 20
                                              Liu H,
                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                              14-JUN-1999;
                                                                                              14-JUN-2000; 2000WO-US16425
                                                                                                                              WO200077486-A2
                                                                                                                                                                                       pallidum acidic repeat protein immunogenic peptide arp 9
                                              Steiner B,
                                                                               99US-0138981.
                                              Rhodes B;
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sample -

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RESULT 2
AAB48317
ID AAB4
 XXXXX
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Best Local
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           The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws,
                                                                                                                                                                                         Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
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                                                                                                                                               Claim 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yaws; bejel.
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                                                                                                                                                                                                                                                                                                           Liu H,
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   bejel
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                                                                                                                                              Fig 8; 73pp; English.
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The immunogenic peptides or the
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Pred. No. 3.1e-09;
; Mismatches 0;
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EVEDVPKVVEPASEREGGER 20

Query Match Best Local S Matches 20

Similarity

100.0%; ilarity 100.0%; Conservative (

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Score 101; DB 2 Pred. No. 7e-08; , Mismatches

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Best Local
                                   The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abb), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. The present sequence represents a T. pallidum subspecies endemicum
                                                                                                                                                                                                                                                              Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                     (USSH )
                             Bosnia)
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                          arp protein.
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312 AA;
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Pred. No. 5e-08;
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AAB48316
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           20-APR-2001
                                     AAB48329
                                                           AAB48329 standard;
                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                              432 AA;
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          (first entry)
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                                                           peptide;
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Pred. No. 1e-07;
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RESULT 6
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                              Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
                                                                                                                                                                         T. pallidum acidic
                                                                                                                                                                                                                                                             AAB48328 standard; peptide; 20
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                                                                                              Treponema pallidum
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                                                                                                                                                                       repeat protein immunogenic peptide arp 10
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Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   T. pallidum acidic repeat protein immunogenic peptide arp
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                   protein of sample -
                                                    Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat
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                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum
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                                                                                                                                        Liu H,
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                                                                                                                                          Rhodes
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95.0%;
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Pred. No. 2e-0
1; Mismatches
                                  an antibody present in
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RESULT 8
AAB48330
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                        The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repark protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting Treponema pallidum in blood, saliva, etc., formation of a complex between immunogenic peptides of protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the protein of the bacterium and an antibody present in the
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arp, as part of an immunoger protective immune response a Sequences AAB48319-AAB48330
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RESULT 9
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100.0%; Pred. No.
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RESULT 11
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           Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
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                                                         T. pallidum acidic repeat protein immunogenic peptide arp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48325 standard; peptide; 21
                                                                                                                                                  AAB48319 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-080711/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                                                              l Similarity
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                                                                                                                                                                                                                                                               VVEPASEREGGER 20
                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                             64.4%; Score 65; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                          DB 22;
0.0019;
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Treponema pallidum.

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RESULT 12
AAB48326
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
 Liu H,
                                                                                                                                                                                  Treponema pallidum; yaws; bejel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1999;
                                                                              14-JUN-2000; 2000WO-US16425.
                                                                                                         21-DEC-2000
                                                                                                                                 WO200077486-A2
                                                                                                                                                        Treponema pallidum.
                                                                                                                                                                                                                       T. pallidum acidic repeat protein immunogenic peptide arp
                                                                                                                                                                                                                                                                                AAB48326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arp protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2000; 2000WO-US16425
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                                                     14-JUN-1999;
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                                                                                                                                                                                                                                                                                                       AAB48326 standard; peptide; 26
                           (USSH ) US DEPT HEALTH & HUMAN
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12; Conservative
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 Steiner B,
                                                                                                                                                                                                                                                                                                                                                                        EVEDAPKVVEPAS 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AA;
                                                                                                                                                                                                                                                    (first entry)
                                                     99US-0138981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0138981.
                                                                                                                                                                                                                                                                                                                                                                                                                                     59.4%;
                                                                                                                                                                                                 acidic repeat protein; arp; immunogenic; syphilis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodes B;
 Rhodes B;
                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 0.011;
0; Mismatches
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RESULT 13
AAG61691
ID AAG61
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Best Local :
              25-FBB-1999

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26-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

11-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological
                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG61691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG61691 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Fig 11; 73pp; English.
                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                  termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AA;
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99US-0127462

99US-0128234

99US-0128714

99US-0129845

99US-0130077

99US-0130077

99US-0130510

99US-0130510

99US-013149

99US-013149

99US-013149
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99US-0123548
                                                                                                                                                      99US-0126785
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Pred. No.
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99US-014336 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0148311 99US-0148311 99US-0148311 99US-0148341 99US-0149368 99US-014923 99US-014923 99US-014923 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-01510	20166 20166
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RESULT 14
AAG16629
AID AAG16629
AC AAG16
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25-FEB-1999

05-MAR-1999

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23-MAR-1999

25-MAR-1999

26-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

17-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; sign hybridisation assay; genetic termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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99US-0160814.
99US-0160815.
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99US-0161406.
99US-0161406.
99US-0161350.
99US-0161360.
99US-0161361.
99US-0161393.
99US-01619920.
99US-01619920.
99US-01619920.
99US-0121825-
99US-012548-
99US-012548-
99US-0125788-
99US-0126785-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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Pred. No. 2.2;
1; Mismatches
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26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999;

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26-APR-1999
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23-APR-1999
24-MAY-1999
30-APR-1999
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31-MAY-1999
11-MAY-1999
                                                                                                                                                                                                                                                                 Protein identification; signa hybridisation assay; genetic termination sequence.
                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                                                       AAG50350;
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                                                                                                                                                                                                                                                                                                                                   standard;
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990S-0161359
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3-0128234

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3-0132485

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S-0125788.
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3-0127462.
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                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                             fragment
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                                                                                                                                                                                                                                                                                             SEQ
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5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                         pathway; metabolic pathway;
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